

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Novo Nordisk A/S
(B) STREET: Novo Alle
(C) CITY: Bagsvaerd
(E) COUNTRY: Denmark
(F) POSTAL CODE (ZIP): 2880
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(H) TELEFAX: +45 4449 3256
(I) TELEX: 37304

(ii) TITLE OF INVENTION: Human Spasmolytic Polypeptide in Glycosylated Form

(iii) NUMBER OF SEQUENCES: 14

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Glu Lys Pro Ser Pro Cys Gln Cys Ser Arg Leu Ser Pro His Asn Arg
1 5 10 15

Thr Asn Cys Gly Phe Pro Gly Ile Thr Ser Asp Gln Cys Phe Asp Asn
20 25 30

29

Gly Cys Cys Phe Asp Ser Ser Val Thr Gly Val Pro Trp Cys Phe His
 35 40 45

Pro Leu Pro Lys Gln Glu Ser Asp Gln Cys Val Met Glu Val Ser Asp
 50 55 60

Arg Arg Asn Cys Gly Tyr Pro Gly Ile Ser Pro Glu Glu Cys Ala Ser
 65 70 75 80

Arg Lys Cys Cys Phe Ser Asn Phe Ile Phe Glu Val Pro Trp Cys Phe
 85 90 95

Phe Pro Asn Ser Val Glu Asp Cys His Tyr
 100 105

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 77..553

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 77..235

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 236..553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GAATTCATT CAAGAATAGT TCAAACAAGA AGATTACAAA CTATCAATTT CATAACAAT 60

ATAAAGACC AAAAGA ATG AAG GCT GTT TTC TTG GTT TTG TCC TTG ATC 109
 Met Lys Ala Val Phe Leu Val Leu Ser Leu Ile
 -53 -50 -45

GGA TTC TGC TGG GCC CAA CCA GTC ACT GGC GAT GAA TCA TCT GTT GAG 157
 Gly Phe Cys Trp Ala Gln Pro Val Thr Gly Asp Glu Ser Ser Val Glu
 -40 -35 -30

30

ATT COG GAA GAG TCT CTG ATC ATC GCT GAA AAC ACC ACT TTG GCT AAC	205
Ile Pro Glu Glu Ser Leu Ile Ile Ala Glu Asn Thr Leu Ala Asn	
-25 -20 -15	
GTC GCC ATG GCT GAG AGA TTG GAG AAG AGA GAG AAA CCC TCC CCC TGC	253
Val Ala Met Ala Glu Arg Leu Glu Lys Arg Glu Lys Pro Ser Pro Cys	
-10 -5 1 5	
CAG TGC TCC AGG CTG AGC CCC CAT AAC AGG ACG AAC TGC GGC TTC OCT	301
Gln Cys Ser Arg Leu Ser Pro His Asn Arg Thr Asn Cys Gly Phe Pro	
10 15 20	
GGA ATC ACC AGT GAC CAG TGT TTT GAC AAT GGA TGC TGT TTC GAC TCC	349
Gly Ile Thr Ser Asp Gln Cys Phe Asp Asn Gly Cys Cys Phe Asp Ser	
25 30 35	
AGT GTC ACT GGG GTC CCC TGG TGT TTC CAC CCC CTC CCA AAG CAA GAG	397
Ser Val Thr Gly Val Pro Trp Cys Phe His Pro Leu Pro Lys Gln Glu	
40 45 50	
TOG GAT CAG TGC GTC ATG GAG GTC TCA GAC AGA AGA AAC TGT GGC TAC	445
Ser Asp Gln Cys Val Met Glu Val Ser Asp Arg Arg Asn Cys Gly Tyr	
55 60 65 70	
COG GGC ATC AGC CCC GAG GAA TGC GGC TCT CGG AAG TGC TGC TTC TCC	493
Pro Gly Ile Ser Pro Glu Glu Cys Ala Ser Arg Lys Cys Cys Phe Ser	
75 80 85	
AAC TTC ATC TTT GAA GTG CCA TGG TGC TTC TTC COG AAC TCT GTG GAA	541
Asn Phe Ile Phe Glu Val Pro Trp Cys Phe Phe Pro Asn Ser Val Glu	
90 95 100	
GAC TGC CAT TAC TAAGTCTAGA	563
Asp Cys His Tyr	
105	

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Lys Ala Val Phe Leu Val Leu Ser Leu Ile Gly Phe Cys Trp Ala	
-53 -50 -45 -40	
Gln Pro Val Thr Gly Asp Glu Ser Ser Val Glu Ile Pro Glu Glu Ser	
-35 -30 -25	
Leu Ile Ile Ala Glu Asn Thr Thr Leu Ala Asn Val Ala Met Ala Glu	
-20 -15 -10	

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Arg Leu Glu Lys Arg Glu Lys Pro Ser Pro Cys Gln Cys Ser Arg Leu
 -5 1 5 10
 Ser Pro His Asn Arg Thr Asn Cys Gly Phe Pro Gly Ile Thr Ser Asp
 15 20 25
 Gln Cys Phe Asp Asn Gly Cys Cys Phe Asp Ser Ser Val Thr Gly Val
 30 35 40
 Pro Trp Cys Phe His Pro Leu Pro Lys Gln Glu Ser Asp Gln Cys Val
 45 50 55
 Met Glu Val Ser Asp Arg Arg Asn Cys Gly Tyr Pro Gly Ile Ser Pro
 60 65 70 75
 Glu Glu Cys Ala Ser Arg Lys Cys Cys Phe Ser Asn Phe Ile Phe Glu
 80 85 90
 Val Pro Trp Cys Phe Phe Pro Asn Ser Val Glu Asp Cys His Tyr
 95 100 105

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: synthetic

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GGCTGAGCCC CCATAACAG

19

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: synthetic

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TGGAAACACC AGGGGAC

17

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: synthetic

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GAGAAACCCCT CCCCCGCGCA GTGCTCCAGG C

31

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: synthetic

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TCAGCCIGGA GCACTGGCAG GGGGAGGGTT TCTC

34

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: synthetic

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GCTGAGAGAT TGGAGAAGAG AGAGAAACCC TCCCCCT

37

- (2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: synthetic

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TGOGTCATGG AGGCTC

17

- (2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: synthetic

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

AGCACCATGG CACTTCAAAG

20

- (2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: synthetic

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GTCCCCCTGGT GTTTCACCC CTTCCCAAAG CAAGAGTCGG ATCAGTGOGT CATGGAGGTC

60

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: synthetic

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

TGAGACCTCC ATGAOCCACT GATCOGACTC TTGCTTTGGG AGGGGGTIGGA AACACCAGGG

60

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: synthetic

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CATGGTGCTT CTTCCGAAC TCTGTGGAAG ACTGCCATTA CTAAGT

46

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs

35

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: synthetic

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CTAGACITAG TAATGGCAGT CTTCCACAGA GTTCGGGAAG AAGCAC

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